09/604,231

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     (FILE 'HOME' ENTERED AT 10:28:20 ON 03 NOV 2004)

     FILE 'STNGUIDE' ENTERED AT 10:28:36 ON 03 NOV 2004

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 10:29:09 ON 03 NOV 2004
L1          3991 S SUGAR (A) PHOSPHOTRANSFERASE?
L2             0 S CORYNEBACTEROIM (A) GLUTAMICUM
L3          7436 S CORYNEBACTERIUM (A) GLUTAMICUM
L4            23 S L1 AND L3
L5            14 DUP REM L4 (9 DUPLICATES REMOVED)
L6         53493 S CORYNEBACTERIUM
L7            29 S L1 AND L6
L8       6771179 S CLON? OR EXPRESS? OR RECOMBINANT
L9            14 S L7 AND L8
L10            8 DUP REM L9 (6 DUPLICATES REMOVED)
                 E POMPEJUS M/AU
L11           85 S E3-E4
                 E KROGER K/AU
                 E KROGER B/AU
L12          132 S E3-E8
                 E SCHRODER H/AU
L13         2098 S E3
                 E ZELDER O/AU
L14          294 S E3-E4
                 E HABERHAUER G/AU
L15          327 S E3-E7
L16         2832 S L11 OR L12 OR L13 OR L14 OR L15
L17            4 S L1 AND L16
L18            3 DUP REM L17 (1 DUPLICATE REMOVED)

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=> s sugar (a) phosphotransferase?
L1          3991 SUGAR (A) PHOSPHOTRANSFERASE?

=> s corynebacteroim (a) glutamicum
L2             0 CORYNEBACTEROIM (A) GLUTAMICUM

=> s corynebacterium (a) glutamicum
L3          7436 CORYNEBACTERIUM (A) GLUTAMICUM

=> s l1 and l3
L4            23 L1 AND L3

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5            14 DUP REM L4 (9 DUPLICATES REMOVED)

=> d 1-14 ibib ab
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L5 ANSWER 1 OF 14 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2004033592 EMBASE

TITLE: Comparative Metabolic Flux Analysis of Lysine-Producing **Corynebacterium glutamicum** Cultured on Glucose or Fructose.

AUTHOR: Kiefer P.; Heinzle E.; Zelder O.; Wittmann C.

CORPORATE SOURCE: C. Wittmann, Biochemical Engineering, Saarland University, Im Stadtwald, 66041 Saarbrucken, Germany. c.wittmann@mx.uni-saarland.de

SOURCE: Applied and Environmental Microbiology, (2004) 70/1 (229-239).
Refs: 22
ISSN: 0099-2240 CODEN: AEMIDF

COUNTRY: United States

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 004 Microbiology

LANGUAGE: English

SUMMARY LANGUAGE: English

AB A comprehensive approach to (13)C tracer studies, labeling measurements by gas chromatography-mass spectrometry, metabolite balancing, and isotopomer modeling, was applied for comparative metabolic network analysis of lysine-producing **Corynebacterium glutamicum** on glucose or fructose. Significantly reduced yields of lysine and biomass and enhanced formation of dihydroxyacetone, glycerol, and lactate in comparison to those for glucose resulted on fructose. Metabolic flux analysis revealed drastic differences in intracellular flux depending on the carbon source applied. On fructose, flux through the pentose phosphate pathway (PPP) was only 14.4% of the total substrate uptake flux and therefore markedly decreased compared to that for glucose (62.0%). This result is due mainly to (i) the predominance of phosphoenolpyruvate-dependent phosphotransferase systems for fructose uptake (PTS(Fructose)) (92.3%), resulting in a major entry of fructose via fructose 1,6-bisphosphate, and (ii) the inactivity of fructose 1,6-bisphosphatase (0.0%). The uptake of fructose during flux via PTS (Mannose) was only 7.7%. In glucose-grown cells, the flux through pyruvate dehydrogenase (70.9%) was much less than that in fructose-grown cells (95.2%). Accordingly, flux through the tricarboxylic acid cycle was decreased on glucose. Normalized to that for glucose uptake, the supply of NADPH during flux was only 112.4% on fructose compared to 176.9% on glucose, which might explain the substantially lower lysine yield of C. glutamicum on fructose. Balancing NADPH levels even revealed an apparent deficiency of NADPH on fructose, which is probably overcome by in vivo activity of malic enzyme. Based on these results, potential targets could be identified for optimization of lysine production by C. glutamicum on fructose, involving (i) modification of flux through the two PTS for fructose uptake, (ii) amplification of fructose 1,6-bisphosphatase to increase flux through the PPP, and (iii) knockout of a not-yet-annotated gene encoding dihydroxyacetone phosphatase or kinase activity to suppress overflow metabolism. Statistical evaluation revealed high precision of the estimates of flux, so the observed differences for metabolic flux are clearly substrate specific.

L5 ANSWER 2 OF 14 BIOTECHDS COPYRIGHT 2004 THE THOMSON CORP. on STN

ACCESSION NUMBER: 2004-02205 BIOTECHDS

TITLE: Production of aromatic amino acid, useful e.g. as pharmaceutical or feed additive, by growing microorganism containing inserted pyruvate carboxylase gene; involving vector-mediated **Corynebacterium glutamicum**, Brevibacterium sp., Bacillus sp., Methanococcus sp., Saccharomyces sp. or Escherichia coli pyruvate carboxylase gene transfer and expression in host cell

AUTHOR: ANDERLEI B; SPRENGER G; SAHM H; BONGAERTS J
PATENT ASSIGNEE: FORSCHUNGSZENTRUM JUELICH GMBH; HOLLAND SWEETENER CO VOF; DSM BIOTECH GMBH
PATENT INFO: WO 2003093490 13 Nov 2003
APPLICATION INFO: WO 2003-DE1380 29 Apr 2003
PRIORITY INFO: DE 2002-1019714 2 May 2002; DE 2002-1019714 2 May 2002
DOCUMENT TYPE: Patent
LANGUAGE: German
AB DERWENT ABSTRACT:

NOVELTY - Microbial production of aromatic amino acids (I), or other metabolites of the (I)-synthesis pathway comprising fermenting a microorganism (A) in which the pyc (pyruvate carboxylase) gene has been inserted, is new.

BIOTECHNOLOGY - Preferred Microorganism: This has an amplified pyc sequence, either as a result of increasing the copy number and/or increasing the level of gene expression. Especially pyc is introduced on a genetic construct. (A) is from e.g. the genera Corynebacterium; Brevibacterium; Bacillus; Methanococcus or Saccharomyces, or particularly it is Escherichia coli. Enzymes that consume phosphoenol pyruvate (PEP), e.g. at least one of PEP carboxylase, PEP-dependent **sugar phosphotransferases** or pyruvate kinase, are 'switched off' or are inactivated, and a PEP-independent transport system for glucose uptake is also introduced into (A). Typically this is a glucose facilitating protein, e.g. from Zymomonas mobilis or a sugar transport gene (transaldolase and/or transketolase) from E. coli. Also the enzymes (3-deoxy-D-arabinoheptulosonate-7-phosphate) DAHP-synthase, shikimate synthase, chorismate mutase and prephenate dehydratase are deregulated and/or strengthened. Preferred Gene: The pyc gene is especially from **Corynebacterium glutamicum**. It is available in plasmid pVWEx-1pyc (J. Mol. Microbiol. Biotechnol., 3 (2001) 295) and a 3.7 kb SphI-HindIII fragment, containing pyc, was cloned into pACYPtac. The recombinant vector, designated pF36 was then used for transformation of host cells.

USE - The method is used to produce Phe (particularly), Tyr or Trp, e.g. for synthesis of the sweetener aspartame, also as pharmaceuticals (or their intermediates) and feed additives; also other metabolites in the biosynthetic pathway to aromatic amino acids, e.g. 3-deoxy-D-arabinoheptulosonate-7-phosphate; shikimic acid; indigo; adipic and benzoic acids etc.

ADVANTAGE - Increasing the pyc gene activity improves production of (I) and other metabolites, by increasing the intracellular availability of phosphoenol pyruvate.

EXAMPLE - The Escherichia coli strain K-12 aroB/pF36 (lacking aroB so unable to form shikimic acid but including the pyruvate carboxylase (pyc) gene on vector pF36) was grown at 37degreesC in presence of isopropyl beta-D-thiogalactopyranoside) for 30 hours. Glucose conversion was then 0.727 mole, with production of 0.074 moles (10.2% on glucose) of 3-deoxy-D-arabino-heptulosonate (X), a precursor of shikimic acid. For a similar strain without the added pyc gene, corresponding figures were 0.459 moles converted and 0.018 moles (X), 4% on glucose, formed. The strain containing pF36 also produced more glutamate (5.4% compared with 2.6%) but less acetate (9% compared with 79.7%). (49 pages)

L5 ANSWER 3 OF 14 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:377040 HCAPLUS
DOCUMENT NUMBER: 138:380496
TITLE: Genes coding for components of the phosphoenolpyruvate-**sugar**-**phosphotransferase** system and their use in engineering of microbial metabolism
INVENTOR(S): Zelder, Oskar; Pompejus, Markus; Schroeder, Hartwig; Kroeger, Burkhard; Klopprogge, Corinna; Haberhauer, Gregor
PATENT ASSIGNEE(S): BASF Aktiengesellschaft, Germany

SOURCE: PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003040357	A2	20030515	WO 2002-EP12140	20021031
WO 2003040357	A3	20031224		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
DE 10154276	A1	20030515	DE 2001-10154276	20011105
EP 1444334	A2	20040811	EP 2002-783045	20021031
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK				

PRIORITY APPLN. INFO.: DE 2001-10154276 A 20011105
WO 2002-EP12140 W 20021031

AB The invention relates to novel nucleic acid mols., the use thereof in the construction of bio-engineered improved microorganisms and to methods for the production of fine chems., especially amino acids with the aid of said bio-engineered improved microorganisms. Genes for components of the phosphoenolpyruvate-**sugar-phosphotransferase** system od **Corynebacterium glutamicum** are identified. The enzymes and genes may be useful in manipulating sugar uptake and metabolism in microorganisms to alter their energy metabolism and fermentation properties (no data.).

L5 ANSWER 4 OF 14 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2003254350 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12777497
TITLE: A single V317A or V317M substitution in Enzyme II of a newly identified beta-glucoside phosphotransferase and utilization system of **Corynebacterium glutamicum** R extends its specificity towards cellobiose.
AUTHOR: Kotrba Pavel; Inui Masayuki; Yukawa Hideaki
CORPORATE SOURCE: Research Institute of Innovative Technology for the Earth, 9-2 Kizugawadai, Kizu, Soraku, Kyoto 619-0292, Japan.
SOURCE: Microbiology (Reading, England), (2003 Jun) 149 (Pt 6) 1569-80.
Journal code: 9430468. ISSN: 1350-0872.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF508972
ENTRY MONTH: 200307
ENTRY DATE: Entered STN: 20030603
Last Updated on STN: 20030801
Entered Medline: 20030731

AB A catabolic system involved in the utilization of beta-glucosides in **Corynebacterium glutamicum** R and its spontaneous mutant variants allowing uptake of cellobiose were investigated. The system

comprises a beta-glucoside-specific Enzyme IIBCA component (gene bglF) of the phosphotransferase system (PTS), a phospho-beta-glucosidase (bglA) and an antiterminator protein (bglG) from the BglG/SacY family of transcription regulators. The results suggest that transcription antitermination is involved in control of induction and carbon catabolite repression of bgl genes, which presumably form an operon. Functional analysis of the bglF and bglA products revealed that they are simultaneously required for uptake, phosphorylation and breakdown of methyl beta-glucoside, salicin and arbutin. Although cellobiose is not normally a substrate for BglF permease and is not utilized by C. glutamicum R, cellobiose-utilizing mutants can be obtained. The mutation responsible was mapped to the bgl locus and sequenced, and point mutations were found in codon 317 of bglF. These led to substitutions V317A and/or V317M near the putative PTS active-site H313 in the membrane-spanning IIC domain of BglF and allowed BglF to act on cellobiose. Such results strengthen the evidence that the IIC domains can be regarded as selectivity filters of the PTS.

L5 ANSWER 5 OF 14 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:673413 HCAPLUS
DOCUMENT NUMBER: 139:380051
TITLE: Osmotic stress, glucose transport capacity and consequences for glutamate overproduction in **Corynebacterium glutamicum**
AUTHOR(S): Gourdon, Pierre; Raherimandimby, Marson; Dominguez, Helene; Cocaign-Bousquet, Muriel; Lindley, Nic D.
CORPORATE SOURCE: Centre de Bioingenierie Gilbert Durand, Laboratoire de Biotechnologie-Bioprocedes, Institut National de Sciences Appliquees, Toulouse, F-31077, Fr.
SOURCE: Journal of Biotechnology (2003), 104(1-3), 77-85
CODEN: JBITD4; ISSN: 0168-1656
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Glucose uptake by **Corynebacterium glutamicum** is predominantly assured by a mannose phosphotransferase system (PTS) with a high affinity for glucose (Km=0.35 mM). Mutants selected for their resistance to 2-deoxyglucose (2DG) and lacking detectable PEP-dependent glucose-transporting activity, retained the capacity to grow on media in which glucose was the only carbon and energy source, albeit at significantly diminished rates, due to the presence of a low affinity (Ks=11 mM) non-PTS uptake system. During growth in media of different osmolarity, specific rates of glucose consumption and of growth of wild type cells were diminished. Cell samples from these cultures were shown to possess similar PTS activities when measured under standard conditions. However, when cells were resuspended in buffer solns. of different osmolarity measurable PTS activity was shown to be dependent upon osmolarity. This inhibition effect was sufficient to account for the decreased rates of both sugar uptake and growth observed in fermentation media of high osmolarity. The secondary glucose transporter was, however, not influenced by medium osmolarity. During industrial fermentation conditions with accumulation of glutamic acid and the corresponding increase in medium osmolarity, similar inhibition of the sugar transport capacity was observed This phenomenon provokes a major process constraint since the decrease in specific rates leads to an increasing proportion of sugar catabolized for maintenance requirements with an associated decrease in product yields.
REFERENCE COUNT: 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 14 BIOTECHDS COPYRIGHT 2004 THE THOMSON CORP. on STN
DUPLICATE 2
ACCESSION NUMBER: 2001-04894 BIOTECHDS

TITLE: **Corynebacterium glutamicum** nucleic acids encoding phosphoenolpyruvate:**sugar phosphotransferase** system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation; selectable marker

AUTHOR: Pompejus M; Kroeger B; Schroeder H; Zelder O; Haberhauer G

PATENT ASSIGNEE: BASF

LOCATION: Ludwigshafen, Germany.

PATENT INFO: WO 2001002583 11 Jan 2001

APPLICATION INFO: WO 2000-DE973 27 Jun 2000

PRIORITY INFO: DE 1999-1042097 3 Sep 1999; US 1999-142691 1 Jul 1999

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2001-080989 [09]

AB Isolated **Corynebacterium glutamicum** ATCC 13032 nucleic acids encoding phosphoenolpyruvate:**sugar-phosphotransferase** system (PTS) proteins or their fragments are claimed. A PTS nucleic acid (N1) does not consist of any of the F-designated genes defined and is selected from one of 17 disclosed nucleic acid sequences (S1) and their fragments nucleic acid which encode a protein selected from one of the 17 protein sequences (S2) disclosed; nucleic acid encoding a naturally occurring allelic variant of a protein selected from (S2). Also claimed are methods for producing the proteins; C. glutamicum PTS protein and its fragments; diagnosis of Corynebacterium diphtheriae infection; fusion proteins; antisense PTS nucleic acid; a method for screening molecules which modulate the activity of a PTS protein; and a transformed host cell. (144pp)

L5 ANSWER 7 OF 14 MEDLINE on STN DUPLICATE 3

ACCESSION NUMBER: 2001700841 MEDLINE

DOCUMENT NUMBER: PubMed ID: 11741338

TITLE: The ptsI gene encoding enzyme I of the phosphotransferase system of **Corynebacterium glutamicum**.

AUTHOR: Kotrba P; Inui M; Yukawa H

CORPORATE SOURCE: Research Institute of Innovative Technology for the Earth, 9-2, Kizugawadai, Kizu-cho, Soraku-gun, Kyoto, 619-0292, Japan.

SOURCE: Biochemical and biophysical research communications, (2001 Dec 21) 289 (5) 1307-13.
Journal code: 0372516. ISSN: 0006-291X.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200202

ENTRY DATE: Entered STN: 20011220
Last Updated on STN: 20020220
Entered Medline: 20020219

AB The phosphoenolpyruvate:carbohydrate phosphotransferase system (PTS) is widespread among bacteria where it mediates carbohydrate uptake and often serves in carbon control. Here we present cloning and analysis of the monocistronic ptsI gene of **Corynebacterium glutamicum** R, which encodes PTS Enzyme I (EI). EI catalyzes the first reaction of PTS and the reported ptsI was shown to complement the corresponding defect in Escherichia coli. The deduced 59.2-kDa EI of 564 amino acids shares more than 50% homology with EIs from Bacillus stearothermophilus, Bacillus subtilis, and Lactobacillus sake. Chromosomal inactivation of ptsI demonstrated that EI plays an indispensable role in PTS of C. glutamicum R and this system represents a dominant sugar uptake system. Cellobiose was only transported and utilized in adaptive mutants of C. glutamicum R. Cellobiose transport was also found to be PTS-dependent and repressed by PTS sugar glucose.

L5 ANSWER 8 OF 14 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2001274434 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11361073
TITLE: **Corynebacterium glutamicum**: a dissection of the PTS.
AUTHOR: Parche S; Burkovski A; Sprenger G A; Weil B; Kramer R; Titgemeyer F
CORPORATE SOURCE: Lehrstuhl fur Mikrobiologie, Friedrich-Alexander-Universitat Erlangen-Nurnberg, Germany.
SOURCE: Journal of molecular microbiology and biotechnology, (2001 Jul) 3 (3) 423-8.
Journal code: 100892561. ISSN: 1464-1801.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20011022
Last Updated on STN: 20011022
Entered Medline: 20011018

AB The high-GC Gram-positive actinomycete **Corynebacterium glutamicum** is commercially exploited as a producer of amino acids that are used as animal feed additives and flavor enhancers. Despite its beneficial role, carbon metabolism and its possible influence on amino acid metabolism is poorly understood. We have addressed this issue by analyzing the phosphotransferase system (PTS), which in many bacteria controls the flux of nutrients and therefore regulates carbon metabolism. The general PTS phosphotransferases enzyme I (EI) and HPr were characterized by demonstration of PEP-dependent phosphotransferase activity. An EI mutant exhibited a pleiotropic negative phenotype in carbon utilization. The role of the PTS as a major sugar uptake system was further demonstrated by the finding that glucose and fructose negative mutants were deficient in the respective enzyme II PTS permease activities. These carbon sources also caused repression of glutamate uptake, which suggests an involvement of the PTS in carbon regulation. The observation that no HPr kinase/phosphatase could be detected suggests that the mechanism of carbon regulation in C. glutamicum is different to the one found in low-GC Gram-positive bacteria.

L5 ANSWER 9 OF 14 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 5
ACCESSION NUMBER: 2000015847 EMBASE
TITLE: Cloning, nucleotide sequencing, and characterization of the ptsG gene encoding glucose-specific enzyme II of the phosphotransferase system from Brevibacterium lactofermentum.
AUTHOR: Yoon K.-H.; Lee K.-N.; Lee J.-K.; Park S.C.
CORPORATE SOURCE: K.-H. Yoon, School of Food Biotechnology, Woosong University, San 7-6, Jayang-Dong, Dong-Gu, Taejon 300-100, Korea, Republic of. ykh@lion.woosong.ac.kr
SOURCE: Journal of Microbiology and Biotechnology, (1999) 9/5 (582-588).
Refs: 31
ISSN: 1017-7825 CODEN: JOMBES
COUNTRY: Korea, Republic of
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB A Brevibacterium lactofermentum gene coding for a glucose-specific permease of the phosphoenolpyruvate-dependent phosphotransferase system (PTS) was cloned, by complementing an Escherichia coli mutation affecting a ptsG gene with the B. lactofermentum genomic library, and completely sequenced. The gene was identified as a ptsG, which enables an E. coli

transformant to transport non-metabolizable glucose analogue 2-deoxyglucose (2DG). The ptsG gene of B. lactofermentum consists of an open reading frame, of 2,025 nucleotides encoding a polypeptide of 674 amino acid residues and a TAA stop codon. The 3' flanking region contains two stem-loop structures which may be involved in transcriptional termination. The deduced amino acid sequence of the B. lactofermentum enzyme II(Glc) specific to glucose (EII(Glc)) has a high homology with the **Corynebacterium glutamicum** enzyme II(Man) specific to glucose and mannose (EII(Man)), and the Brevibacterium ammoniagenes enzyme II(Glc) specific to glucose (EII(Glc)). The 171-amino-acid C-terminal sequence of the EII(Glc) is also similar to the Escherichia coli enzyme IIA(Glc) specific to glucose (IIA(Glc)). It is interesting that the arrangement of the structural domains, IIBCA, of the B. lactofermentum EII(Glc) protein is identical to that of EIIs specific to sucrose or β- glucoside. Several in vivo complementation studies indicated that the B. lactofermentum EII(Glc) protein could replace both EII(Glc) and EIIA(Glc) in an E. coli ptsG mutant or crr mutant, respectively.

L5 ANSWER 10 OF 14 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:714378 HCAPLUS
DOCUMENT NUMBER: 130:109230
TITLE: L-Lysine experimental yields by **Corynebacterium glutamicum** on carbon substrates
AUTHOR(S): Ruklisha, M.; Ionina, R.
CORPORATE SOURCE: Institute of Microbiology and Biotechnology, University of Latvia, Riga, LV-1586, Latvia
SOURCE: Mededelingen - Faculteit Landbouwkundige en Toegepaste Biologische Wetenschappen (Universiteit Gent) (1998), 63(4a), 1341-1344
CODEN: MFLBER; ISSN: 1373-7503
PUBLISHER: Universiteit Gent, Faculteit Landbouwkundige en Toegepaste Biologische Wetenschappen
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Growth of C. glutamicum and C. flavum on different carbon and energy substrates was investigated to determine the advantages of definitive substrates for increasing lysine production and to identify rate-limiting metabolic steps. The impact of the C source on the growth rate, sugar uptake, lysine yield, and catabolic and lysine-synthesizing enzyme activities was determined Sucrose was the best C source for increased lysine prodn; an equimolar mix. of glucose and fructose was effective also. The observed metabolic differences resulted in differences in metabolite overflow in the direction of lysine synthesis.
REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 11 OF 14 MEDLINE on STN
ACCESSION NUMBER: 1998314508 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9652400
TITLE: Carbon-flux distribution in the central metabolic pathways of **Corynebacterium glutamicum** during growth on fructose.
AUTHOR: Dominguez H; Rollin C; Guyonvarch A; Guerquin-Kern J L; Cocaign-Bousquet M; Lindley N D
CORPORATE SOURCE: Centre de Bioingenierie Gilbert Durand, UMR CNRS/INSA & L.A. INRA, Institut National des Sciences Appliquees, Complexe Scientifique de Rangueil, Toulouse, France.
SOURCE: European journal of biochemistry / FEBS, (1998 May 15) 254 (1) 96-102.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980811
Last Updated on STN: 19990129
Entered Medline: 19980728

AB Growth of **Corynebacterium glutamicum** on fructose was significantly less than that obtained on glucose, despite similar rates of substrate uptake. This was in part due to the production of overflow metabolites (dihydroxyacetone and lactate) but also to the increased production of CO2 during growth on fructose. These differences in carbon-metabolite accumulation are indicative of a different pattern of carbon-flux distribution through the central metabolic pathways. Growth on glucose has been previously shown to involve a high flux (> 50% of total glucose consumption) via the pentose pathway to generate anabolic reducing equivalents. NMR analysis of carbon-isotope distribution patterns of the glutamate pool after growth on 1-13C- or 6-13C-enriched fructose indicates that the contribution of the pentose pathway is significantly diminished during exponential growth on fructose with glycolysis being the predominant pathway (80% of total fructose consumption). The increased flux through glycolysis during growth on fructose is associated with an increased NADH/NAD+ ratio susceptible to inhibit both glyceraldehyde-3-phosphate dehydrogenase and pyruvate dehydrogenase, and provoking the overflow of metabolites derived from the substrates of these two enzymes. The biomass yield observed experimentally is higher than can be estimated from the apparent quantity of NADPH associated with the pentose pathway and the flux through isocitrate dehydrogenase, suggesting an additional reaction yielding NADPH. This may involve a modified tricarboxylic acid cycle involving malic enzyme, expressed to significantly higher levels during growth on fructose than on glucose, and a pyruvate carboxylating anaplerotic enzyme.

L5 ANSWER 12 OF 14 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:184754 HCAPLUS
DOCUMENT NUMBER: 128:292608
TITLE: Determination of the carbon flux in the central metabolism of **Corynebacterium glutamicum** by 13C-isotope analysis
AUTHOR(S): Marx, Achim
CORPORATE SOURCE: Inst. Biotechnologie, Forschungszentrum Juelich G.m.b.H., Juelich, D-52425, Germany
SOURCE: Berichte des Forschungszentrums Juelich (1997), Juel-3459, 1-111 pp.
CODEN: FJBEE5; ISSN: 0366-0885
DOCUMENT TYPE: Report
LANGUAGE: German

AB All C fluxes of the central metabolism of C. glutamicum were quantified and the role and coordination of single metabolic pathways were studied under different metabolic situations. A method based on 13C-data was established to quantify all metabolite fluxes of the central metabolism Strong sensitivities were indicated between metabolic fluxes and 13C data, thus allowing the determination of metabolite flux. When the 13C-content of the position oxalacetate C-4 was varied by the factor 2 it could be shown if anaplerotic production of C4-bodies was via the carboxylation of C3-bodies or via the glyoxalate cycle. A hyperbolic relationship was shown for the bi-directional turnover of transketolase and the 13C-content of the position pentose-5-phosphate C-1 and for the bi-directional metabolite flux between C3-bodies of glycolysis and C4-bodies of the tricarboxylate (TCA) cycle and 13C-enrichment of the position oxalacetate C-2. The NADPH balance showed that, depending on the conditions, more NADPH was produced than necessary for the synthesis of biomass and products. The NADPH excess was 16-67% in relation to the glucose uptake rate. Depending on the metabolic situation, the C4-body-decarboxylation was 10-132% and opposed to the carboxylation of C3-bodies for the anaplerotic supply of

the TCA cycle. C4-body-decarboxylation and NADPH-excess as adaptations to high production of Lys were minimal, with a yield coefficient of 0.32 molLysmolglucose-1. The contribution of malate enzyme to a total NADPH production of 211% was small. The pentose phosphate pathway (PPP) and the TCA cycle produced 3/4 and 1/4, resp., of the total NADPH. Overexpression of glutamate dehydrogenase in a mutant of strain MH20-22B resulted in low TCA cycle flux and a high metabolite flux through the oxidative PPP. A high TCA cycle flux was detected during glutamate production using strain LE4. The PPP flux was low in this strain. In a mutant of strain MH20-22B producing Lys and using NADH for synthesis of glutamate, TCA cycle flux was 79% and that of PPP was 26%. The low PPP was due to low NADPH consumption and high NADPH production from isocitrate dehydrogenase of the TCA cycle. A strain ATCC 13032 isocitrate dehydrogenase mutant with a blocked TCA cycle showed a PPP flux of 62%. This mutant showed a glyoxalate cycle active in vivo when metabolizing glucose. This metabolite flux was 53%. A flux of 16% produced anaplerotically C4-bodies. At a flux of 37% the glyoxalate cycle released CO2 by C4-body decarboxylation and pyruvate dehydrogenase.

L5 ANSWER 13 OF 14 MEDLINE on STN DUPLICATE 6
ACCESSION NUMBER: 94314161 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8039653
TITLE: Nucleotide sequence of the gene encoding the **Corynebacterium glutamicum** mannose enzyme II and analyses of the deduced protein sequence.
AUTHOR: Lee J K; Sung M H; Yoon K H; Yu J H; Oh T K
CORPORATE SOURCE: Genetic Engineering Research Institute, Korea Institute of Science and Technology, Yusung, Taejon, South Korea.
SOURCE: FEMS microbiology letters, (1994 Jun 1) 119 (1-2) 137-45. Journal code: 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L18874
ENTRY MONTH: 199408
ENTRY DATE: Entered STN: 19940905
Last Updated on STN: 19940905
Entered Medline: 19940825

AB The complete nucleotide sequence of the gene encoding the **Corynebacterium glutamicum** mannose enzyme II (EIIMan) was determined. The gene consisted of 2052 base pairs encoding a protein of 683 amino acid residues; the molecular mass of the protein subunit was calculated to be 72570 Da. The N-terminal hydrophilic domain of EIIMan showed 39.7% homology with a C-terminal hydrophilic domain of Escherichia coli glucose-specific enzyme II (EIIGlc). Similar homology was shown between the C-terminal sequence of EIIMan and the E. coli glucose-specific enzyme III (EIIIGlc), or the EIII-like domain of Streptococcus mutans sucrose-specific enzyme II. Sequence comparison with other EIIs showed that EIIMan contained residues His-602 and Cys-28 which were homologous to the potential phosphorylation sites of EIIIGlc, or EIII-like domains, and hydrophilic domains (IIB) of several EIIs, respectively.

L5 ANSWER 14 OF 14 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
ACCESSION NUMBER: 1993:482699 BIOSIS
DOCUMENT NUMBER: PREV199396116299
TITLE: Characterization of phosphoenolpyruvate carboxykinase from **Corynebacterium glutamicum**.
AUTHOR(S): Jetten, Mike S. M. [Reprint author]; Sinskey, Anthony J.
CORPORATE SOURCE: Dep. Biol., Room 16-238, Mass. Inst. Technol., 77 Massachusetts Ave., Cambridge, MA 02139, USA
SOURCE: FEMS (Federation of European Microbiological Societies) Microbiology Letters, (1993) Vol. 111, No. 2-3, pp. 183-188.

CODEN: FMLED7. ISSN: 0378-1097.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 22 Oct 1993
Last Updated on STN: 23 Oct 1993

AB Phosphoenolpyruvate (PEP) carboxykinase is present in crude extracts of **Corynebacterium glutamicum** grown on both glucose and lactate. Preparation of PEP carboxykinase free from interfering PEP carboxylase and oxaloacetate decarboxylase showed an absolute dependence on divalent manganese and IDP for activity in the oxaloacetate (OAA) formation. Other diphosphate nucleotides could not substitute for IDP. The enzyme activity displayed Michaelis-Menten kinetics for the substrates PEP, IDP, KHCO-3, OAA and ITP with a K-m of 0.7 mM, 0.4 mM, 12 mM, 1.0 mM, and 0.5 mM, respectively. At the optimum pH of 6.6, 850 nmol of OAA were formed per min per mg of protein. ATP inhibited PEP carboxykinase in the OAA forming reaction for 60% at 0.1 mM, indicating that the enzyme mainly functions in gluconeogenesis.

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=> d his

     (FILE 'HOME' ENTERED AT 10:28:20 ON 03 NOV 2004)

     FILE 'STNGUIDE' ENTERED AT 10:28:36 ON 03 NOV 2004

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 10:29:09 ON 03 NOV 2004
L1          3991 S SUGAR (A) PHOSPHOTRANSFERASE?
L2             0 S CORYNEBACTEROIM (A) GLUTAMICUM
L3          7436 S CORYNEBACTERIUM (A) GLUTAMICUM
L4            23 S L1 AND L3
L5            14 DUP REM L4 (9 DUPLICATES REMOVED)

=> s corynebacterium
L6         53493 CORYNEBACTERIUM

=> s l1 and l6
L7            29 L1 AND L6

=> s clon? or express? or recombinant
   3 FILES SEARCHED...
L8       6771179 CLON? OR EXPRESS? OR RECOMBINANT

=> s l7 and l8
L9            14 L7 AND L8

=> dup rem l9
PROCESSING COMPLETED FOR L9
L10            8 DUP REM L9 (6 DUPLICATES REMOVED)

=> d 1-8 ibib ab

L10   ANSWER 1 OF 8  BIOTECHDS COPYRIGHT 2004 THE THOMSON CORP. on STN
ACCESSION NUMBER: 2004-02205  BIOTECHDS
TITLE:            Production of aromatic amino acid, useful e.g. as
                  pharmaceutical or feed additive, by growing microorganism
                  containing inserted pyruvate carboxylase gene;
                     involving vector-mediated Corynebacterium
                     glutamicum, Brevibacterium sp., Bacillus sp.,
                     Methanococcus sp., Saccharomyces sp. or Escherichia coli
                     pyruvate carboxylase gene transfer and expression
                     in host cell
AUTHOR:           ANDERLEI B; SPRENGER G; SAHM H; BONGAERTS J
PATENT ASSIGNEE:  FORSCHUNGSZENTRUM JUELICH GMBH; HOLLAND SWEETENER CO VOF; DSM
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BIOTECH GMBH
PATENT INFO: WO 2003093490 13 Nov 2003
APPLICATION INFO: WO 2003-DE1380 29 Apr 2003
PRIORITY INFO: DE 2002-1019714 2 May 2002; DE 2002-1019714 2 May 2002
DOCUMENT TYPE: Patent
LANGUAGE: German
AB DERWENT ABSTRACT:

NOVELTY - Microbial production of aromatic amino acids (I), or other metabolites of the (I)-synthesis pathway comprising fermenting a microorganism (A) in which the pyc (pyruvate carboxylase) gene has been inserted, is new.

BIOTECHNOLOGY - Preferred Microorganism: This has an amplified pyc sequence, either as a result of increasing the copy number and/or increasing the level of gene **expression**. Especially pyc is introduced on a genetic construct. (A) is from e.g. the genera **Corynebacterium**; Brevibacterium; Bacillus; Methanococcus or Saccharomyces, or particularly it is Escherichia coli. Enzymes that consume phosphoenol pyruvate (PEP), e.g. at least one of PEP carboxylase, PEP-dependent **sugar phosphotransferases** or pyruvate kinase, are 'switched off' or are inactivated, and a PEP-independent transport system for glucose uptake is also introduced into (A). Typically this is a glucose facilitating protein, e.g. from Zymomonas mobilis or a sugar transport gene (transaldolase and/or transketolase) from E. coli. Also the enzymes (3-deoxy-D-arabinoheptulosonate-7-phosphate) DAHP-synthase, shikimate synthase, chorismate mutase and prephenate dehydratase are deregulated and/or strengthened. Preferred Gene: The pyc gene is especially from **Corynebacterium** glutamicum. It is available in plasmid pVWEx-1pyc (J. Mol. Microbiol. Biotechnol., 3 (2001) 295) and a 3.7 kb SphI-HindIII fragment, containing pyc, was **cloned** into pACYPtac. The **recombinant** vector, designated pF36 was then used for transformation of host cells.

USE - The method is used to produce Phe (particularly), Tyr or Trp, e.g. for synthesis of the sweetener aspartame, also as pharmaceuticals (or their intermediates) and feed additives; also other metabolites in the biosynthetic pathway to aromatic amino acids, e.g. 3-deoxy-D-arabinoheptulosonate-7-phosphate; shikimic acid; indigo; adipic and benzoic acids etc.

ADVANTAGE - Increasing the pyc gene activity improves production of (I) and other metabolites, by increasing the intracellular availability of phosphoenol pyruvate.

EXAMPLE - The Escherichia coli strain K-12 aroB/pF36 (lacking aroB so unable to form shikimic acid but including the pyruvate carboxylase (pyc) gene on vector pF36) was grown at 37degreesC in presence of isopropyl beta-D-thiogalactopyranoside) for 30 hours. Glucose conversion was then 0.727 mole, with production of 0.074 moles (10.2% on glucose) of 3-deoxy-D-arabino-heptulosonate (X), a precursor of shikimic acid. For a similar strain without the added pyc gene, corresponding figures were 0.459 moles converted and 0.018 moles (X), 4% on glucose, formed. The strain containing pF36 also produced more glutamate (5.4% compared with 2.6%) but less acetate (9% compared with 79.7%). (49 pages)

L10 ANSWER 2 OF 8 MEDLINE on STN
ACCESSION NUMBER: 2003254350 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12777497
TITLE: A single V317A or V317M substitution in Enzyme II of a newly identified beta-glucoside phosphotransferase and utilization system of **Corynebacterium** glutamicum R extends its specificity towards cellobiose.
AUTHOR: Kotrba Pavel; Inui Masayuki; Yukawa Hideaki
CORPORATE SOURCE: Research Institute of Innovative Technology for the Earth, 9-2 Kizugawadai, Kizu, Soraku, Kyoto 619-0292, Japan.
SOURCE: Microbiology (Reading, England), (2003 Jun) 149 (Pt 6) 1569-80.
Journal code: 9430468. ISSN: 1350-0872.

PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF508972
ENTRY MONTH: 200307
ENTRY DATE: Entered STN: 20030603
Last Updated on STN: 20030801
Entered Medline: 20030731

AB A catabolic system involved in the utilization of beta-glucosides in **Corynebacterium** glutamicum R and its spontaneous mutant variants allowing uptake of cellobiose were investigated. The system comprises a beta-glucoside-specific Enzyme IIBCA component (gene bglF) of the phosphotransferase system (PTS), a phospho-beta-glucosidase (bglA) and an antiterminator protein (bglG) from the BglG/SacY family of transcription regulators. The results suggest that transcription antitermination is involved in control of induction and carbon catabolite repression of bgl genes, which presumably form an operon. Functional analysis of the bglF and bglA products revealed that they are simultaneously required for uptake, phosphorylation and breakdown of methyl beta-glucoside, salicin and arbutin. Although cellobiose is not normally a substrate for BglF permease and is not utilized by C. glutamicum R, cellobiose-utilizing mutants can be obtained. The mutation responsible was mapped to the bgl locus and sequenced, and point mutations were found in codon 317 of bglF. These led to substitutions V317A and/or V317M near the putative PTS active-site H313 in the membrane-spanning IIC domain of BglF and allowed BglF to act on cellobiose. Such results strengthen the evidence that the IIC domains can be regarded as selectivity filters of the PTS.

L10 ANSWER 3 OF 8 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:31659 HCAPLUS
DOCUMENT NUMBER: 134:96287
TITLE: **Corynebacterium** glutamicum genes encoding phosphoenolpyruvate:**sugar** **phosphotransferase** system proteins
INVENTOR(S): Pompejus, Markus; Kroger, Burkhard; Schroder, Hartwig; Zelder, Oskar; Haberhauer, Gregor
PATENT ASSIGNEE(S): BASF Aktiengesellschaft, Germany
SOURCE: PCT Int. Appl., 143 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 9
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001002583	A2	20010111	WO 2000-IB973	20000627
WO 2001002583	A3	20010726		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2000057014	A5	20010122	AU 2000-57014	20000627
TR 200103854	T2	20020621	TR 2001-200103854	20000627
BR 2000012038	A	20020702	BR 2000-12038	20000627
EP 1246922	A2	20021009	EP 2000-942322	20000627
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				

JP 2003512024	T2	20030402	JP 2001-508355		20000627
US 2004180408	A1	20040916	US 2004-781014		20040217
PRIORITY APPLN. INFO.:			US 1999-142691P	P	19990701
			US 1999-150310P	P	19990823
			DE 1999-19942095	A	19990903
			DE 1999-19942097	A	19990903
			US 1999-141031P	P	19990625
			DE 1999-19931412	A	19990708
			DE 1999-19931413	A	19990708
			DE 1999-19931419	A	19990708
			DE 1999-19931420	A	19990708
			DE 1999-19931424	A	19990708
			DE 1999-19931428	A	19990708
			DE 1999-19931431	A	19990708
			DE 1999-19931433	A	19990708
			DE 1999-19931434	A	19990708
			DE 1999-19931510	A	19990708
			DE 1999-19931562	A	19990708
			DE 1999-19931634	A	19990708
			DE 1999-19932180	A	19990709
			DE 1999-19932227	A	19990709
			DE 1999-19932230	A	19990709
			US 1999-143208P	P	19990709
			DE 1999-19932924	A	19990714
			DE 1999-19932973	A	19990714
			DE 1999-19933005	A	19990714
			DE 1999-19940765	A	19990827
			US 1999-151572P	P	19990831
			DE 1999-19942076	A	19990903
			DE 1999-19942079	A	19990903
			DE 1999-19942086	A	19990903
			DE 1999-19942087	A	19990903
			DE 1999-19942088	A	19990903
			DE 1999-19942123	A	19990903
			DE 1999-19942125	A	19990903
			US 2000-602740	A1	20000623
			WO 2000-IB973	W	20000627

AB Isolated nucleic acid mols., designated phosphoenolpyruvate:**sugar phosphotransferase** (PTS) nucleic acid mols., which encode novel PTS proteins from **Corynebacterium** glutamicum are described. The invention also provides antisense nucleic acid mols., **recombinant expression** vectors containing PTS nucleic acid mols., and host cells into which the **expression** vectors have been introduced. The invention still further provides isolated PTS proteins, mutated PTS proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from C. glutamicum based on genetic engineering of PTS genes in this organism.

L10 ANSWER 4 OF 8 MEDLINE on STN

ACCESSION NUMBER: 2001331960 MEDLINE

DOCUMENT NUMBER: PubMed ID: 11287431

TITLE: Evidence for direct interaction between enzyme I(Ntr) and aspartokinase to regulate bacterial oligopeptide transport.

AUTHOR: King N D; O'Brian M R

CORPORATE SOURCE: Department of Biochemistry and Center for Microbial Pathogenesis, State University of New York at Buffalo, Buffalo, New York 14214, USA.

SOURCE: Journal of biological chemistry, (2001 Jun 15) 276 (24) 21311-6.
Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF323675
ENTRY MONTH: 200107
ENTRY DATE: Entered STN: 20010723
Last Updated on STN: 20030105
Entered Medline: 20010719

AB Bradyrhizobium japonicum transports oligopeptides and the heme precursor delta-aminolevulinic acid (ALA) by a common mechanism. Two Tn5-induced mutants disrupted in the lysC and ptsP genes were identified based on the inability to use prolyl-glycyl-glycine as a proline source and were defective in [(14)C]ALA uptake activity. lysC and ptsP were shown to be proximal genes in the B. japonicum genome. However, RNase protection and in trans complementation analysis showed that lysC and ptsP are transcribed separately, and that both genes are involved in oligopeptide transport. Aspartokinase, encoded by lysC, catalyzes the phosphorylation of aspartate for synthesis of three amino acids, but the lysC strain is not an amino acid auxotroph. The ptsP gene encodes Enzyme I(Ntr) (EI(Ntr)), a paralogue of Enzyme I of the phosphoenolpyruvate: **sugar phosphotransferase** (PTS) system. In vitro pull-down experiments indicated that purified **recombinant** aspartokinase and EI(Ntr) interact directly with each other. **Expression** of ptsP in trans from a multicopy plasmid complemented the lysC mutant, suggesting that aspartokinase normally affects Enzyme I(Ntr) in a manner that can be compensated for by increasing the copy number of the ptsP gene. ATP was not a phosphoryl donor to purified EI(Ntr), but it was phosphorylated by ATP in the presence of cell extracts. This phosphorylation was inhibited in the presence of aspartokinase. The findings demonstrate a role for a PTS protein in the transport of a non-sugar solute and suggest an unusual regulatory function for aspartokinase in regulating the phosphorylation state of EI(Ntr).

L10 ANSWER 5 OF 8 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2001700841 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11741338
TITLE: The ptsI gene encoding enzyme I of the phosphotransferase system of **Corynebacterium** glutamicum.
AUTHOR: Kotrba P; Inui M; Yukawa H
CORPORATE SOURCE: Research Institute of Innovative Technology for the Earth, 9-2, Kizugawadai, Kizu-cho, Soraku-gun, Kyoto, 619-0292, Japan.
SOURCE: Biochemical and biophysical research communications, (2001 Dec 21) 289 (5) 1307-13.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011220
Last Updated on STN: 20020220
Entered Medline: 20020219

AB The phosphoenolpyruvate:carbohydrate phosphotransferase system (PTS) is widespread among bacteria where it mediates carbohydrate uptake and often serves in carbon control. Here we present **cloning** and analysis of the monocistronic ptsI gene of **Corynebacterium** glutamicum R, which encodes PTS Enzyme I (EI). EI catalyzes the first reaction of PTS and the reported ptsI was shown to complement the corresponding defect in Escherichia coli. The deduced 59.2-kDa EI of 564 amino acids shares more than 50% homology with EIs from Bacillus stearothermophilus, Bacillus subtilis, and Lactobacillus sake. Chromosomal inactivation of ptsI demonstrated that EI plays an indispensable role in PTS of C. glutamicum R and this system represents a dominant sugar uptake system. Cellobiose was only transported and utilized in adaptive mutants of C. glutamicum R. Cellobiose transport was also found to be PTS-dependent and repressed by PTS sugar glucose.

L10 ANSWER 6 OF 8 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN DUPLICATE 2
ACCESSION NUMBER: 2000015847 EMBASE
TITLE: **Cloning**, nucleotide sequencing, and characterization of the ptsG gene encoding glucose-specific enzyme II of the phosphotransferase system from Brevibacterium lactofermentum.
AUTHOR: Yoon K.-H.; Lee K.-N.; Lee J.-K.; Park S.C.
CORPORATE SOURCE: K.-H. Yoon, School of Food Biotechnology, Woosong University, San 7-6, Jayang-Dong, Dong-Gu, Taejon 300-100, Korea, Republic of. ykh@lion.woosong.ac.kr
SOURCE: Journal of Microbiology and Biotechnology, (1999) 9/5 (582-588).
Refs: 31
ISSN: 1017-7825 CODEN: JOMBES
COUNTRY: Korea, Republic of
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB A Brevibacterium lactofermentum gene coding for a glucose-specific permease of the phosphoenolpyruvate-dependent phosphotransferase system (PTS) was **cloned**, by complementing an Escherichia coli mutation affecting a ptsG gene with the B. lactofermentum genomic library, and completely sequenced. The gene was identified as a ptsG, which enables an E. coli transformant to transport non-metabolizable glucose analogue 2-deoxyglucose (2DG). The ptsG gene of B. lactofermentum consists of an open reading frame, of 2,025 nucleotides encoding a polypeptide of 674 amino acid residues and a TAA stop codon. The 3' flanking region contains two stem-loop structures which may be involved in transcriptional termination. The deduced amino acid sequence of the B. lactofermentum enzyme II(Glc) specific to glucose (EII(Glc)) has a high homology with the **Corynebacterium** glutamicum enzyme II(Man) specific to glucose and mannose (EII(Man)), and the Brevibacterium ammoniagenes enzyme II(Glc) specific to glucose (EII(Glc)). The 171-amino-acid C-terminal sequence of the EII(Glc) is also similar to the Escherichia coli enzyme IIA(Glc) specific to glucose (IIA(Glc)). It is interesting that the arrangement of the structural domains, IIBCA, of the B. lactofermentum EII(Glc) protein is identical to that of EIIs specific to sucrose or β- glucoside. Several in vivo complementation studies indicated that the B. lactofermentum EII(Glc) protein could replace both EII(Glc) and EIIA(Glc) in an E. coli ptsG mutant or crr mutant, respectively.

L10 ANSWER 7 OF 8 MEDLINE on STN
ACCESSION NUMBER: 1998314508 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9652400
TITLE: Carbon-flux distribution in the central metabolic pathways of **Corynebacterium** glutamicum during growth on fructose.
AUTHOR: Dominguez H; Rollin C; Guyonvarch A; Guerquin-Kern J L; Cocaign-Bousquet M; Lindley N D
CORPORATE SOURCE: Centre de Bioingenierie Gilbert Durand, UMR CNRS/INSA & L.A. INRA, Institut National des Sciences Appliquees, Complexe Scientifique de Rangueil, Toulouse, France.
SOURCE: European journal of biochemistry / FEBS, (1998 May 15) 254 (1) 96-102.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980811

Last Updated on STN: 19990129
Entered Medline: 19980728

AB Growth of **Corynebacterium** glutamicum on fructose was significantly less than that obtained on glucose, despite similar rates of substrate uptake. This was in part due to the production of overflow metabolites (dihydroxyacetone and lactate) but also to the increased production of CO2 during growth on fructose. These differences in carbon-metabolite accumulation are indicative of a different pattern of carbon-flux distribution through the central metabolic pathways. Growth on glucose has been previously shown to involve a high flux (> 50% of total glucose consumption) via the pentose pathway to generate anabolic reducing equivalents. NMR analysis of carbon-isotope distribution patterns of the glutamate pool after growth on 1-13C- or 6-13C-enriched fructose indicates that the contribution of the pentose pathway is significantly diminished during exponential growth on fructose with glycolysis being the predominant pathway (80% of total fructose consumption). The increased flux through glycolysis during growth on fructose is associated with an increased NADH/NAD+ ratio susceptible to inhibit both glyceraldehyde-3-phosphate dehydrogenase and pyruvate dehydrogenase, and provoking the overflow of metabolites derived from the substrates of these two enzymes. The biomass yield observed experimentally is higher than can be estimated from the apparent quantity of NADPH associated with the pentose pathway and the flux through isocitrate dehydrogenase, suggesting an additional reaction yielding NADPH. This may involve a modified tricarboxylic acid cycle involving malic enzyme, **expressed** to significantly higher levels during growth on fructose than on glucose, and a pyruvate carboxylating anaplerotic enzyme.

L10 ANSWER 8 OF 8 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 94314161 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8039653
TITLE: Nucleotide sequence of the gene encoding the **Corynebacterium** glutamicum mannose enzyme II and analyses of the deduced protein sequence.
AUTHOR: Lee J K; Sung M H; Yoon K H; Yu J H; Oh T K
CORPORATE SOURCE: Genetic Engineering Research Institute, Korea Institute of Science and Technology, Yusung, Taejon, South Korea.
SOURCE: FEMS microbiology letters, (1994 Jun 1) 119 (1-2) 137-45. Journal code: 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L18874
ENTRY MONTH: 199408
ENTRY DATE: Entered STN: 19940905
Last Updated on STN: 19940905
Entered Medline: 19940825

AB The complete nucleotide sequence of the gene encoding the **Corynebacterium** glutamicum mannose enzyme II (EIIMan) was determined. The gene consisted of 2052 base pairs encoding a protein of 683 amino acid residues; the molecular mass of the protein subunit was calculated to be 72570 Da. The N-terminal hydrophilic domain of EIIMan showed 39.7% homology with a C-terminal hydrophilic domain of Escherichia coli glucose-specific enzyme II (EIIGlc). Similar homology was shown between the C-terminal sequence of EIIMan and the E. coli glucose-specific enzyme III (EIIIGlc), or the EIII-like domain of Streptococcus mutans sucrose-specific enzyme II. Sequence comparison with other EIIs showed that EIIMan contained residues His-602 and Cys-28 which were homologous to the potential phosphorylation sites of EIIIGlc, or EIII-like domains, and hydrophilic domains (IIB) of several EIIs, respectively.

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=> d his

     (FILE 'HOME' ENTERED AT 10:28:20 ON 03 NOV 2004)

     FILE 'STNGUIDE' ENTERED AT 10:28:36 ON 03 NOV 2004

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 10:29:09 ON 03 NOV 2004
L1          3991 S SUGAR (A) PHOSPHOTRANSFERASE?
L2             0 S CORYNEBACTEROIM (A) GLUTAMICUM
L3          7436 S CORYNEBACTERIUM (A) GLUTAMICUM
L4            23 S L1 AND L3
L5            14 DUP REM L4 (9 DUPLICATES REMOVED)
L6         53493 S CORYNEBACTERIUM
L7            29 S L1 AND L6
L8       6771179 S CLON? OR EXPRESS? OR RECOMBINANT
L9            14 S L7 AND L8
L10            8 DUP REM L9 (6 DUPLICATES REMOVED)

=> e pompejus ma/u
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'EMBASE'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'SCISEARCH'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'BIOSIS'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'MEDLINE'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'LIFESCI'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'HCAPLUS'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'NTIS'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'BIOTECHDS'
The indicated field code is not available for EXPAND in this
file.  To see a list of valid EXPAND field codes, enter HELP
SFIELDS at an arrow prompt (=>).

=> e pompejus m/u
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'SCISEARCH'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'BIOSIS'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'MEDLINE'
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'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'HCAPLUS'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'BIOTECHDS'
'U' IS NOT A VALID EXPAND FIELD CODE FOR FILE 'NTIS'
The indicated field code is not available for EXPAND in this
file.  To see a list of valid EXPAND field codes, enter HELP
SFIELDS at an arrow prompt (=>).

=> e pompejus m/au
E1            42      POMPEIUS R/AU
E2             2      POMPEJUS GERHARD/AU
E3            43 --> POMPEJUS M/AU
E4            42      POMPEJUS MARKUS/AU
E5            37      POMPEKIRN V/AU
E6             1      POMPEL M/AU
E7             1      POMPEL P/AU
E8             1      POMPELEAN A/AU
E9             1      POMPELIA D MICK/AU
E10            2      POMPELIA DONALD M/AU
E11            2      POMPELIANO O/AU
E12          247      POMPELLA A/AU

=> s e3-e4
L11           85 ("POMPEJUS M"/AU OR "POMPEJUS MARKUS"/AU)

=> e kroger k/au
E1             5      KROGER JORG/AU
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E2            2      KROGER JYRKI/AU
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E4            2      KROGER K H/AU
E5            1      KROGER KARL/AU
E6            2      KROGER KERSTIN/AU
E7           13      KROGER KNUT/AU
E8           64      KROGER L/AU
E9          171      KROGER L A/AU
E10           1      KROGER L E/AU
E11           1      KROGER LARRY ALLAN/AU
E12           6      KROGER LARS/AU

=> e kroger b/au
E1            2      KROGER ANJA/AU
E2            1      KROGER ANNELENE/AU
E3           98 --> KROGER B/AU
E4           10      KROGER B J/AU
E5            1      KROGER BERND/AU
E6            1      KROGER BERNHARD/AU
E7            4      KROGER BLOCK A/AU
E8           18      KROGER BURKHARD/AU
E9          100      KROGER C/AU
E10          21      KROGER C F/AU
E11           2      KROGER C J/AU
E12           1      KROGER C R/AU

=> s e3-e8
L12         132 ("KROGER B"/AU OR "KROGER B J"/AU OR "KROGER BERND"/AU OR "KROGE
                R BERNHARD"/AU OR "KROGER BLOCK A"/AU OR "KROGER BURKHARD"/AU)

=> e schroder h/au
E1            1      SCHRODER GUSTAV ADOLF/AU
E2            1      SCHRODER GUY/AU
E3         2098 --> SCHRODER H/AU
E4           53      SCHRODER H A/AU
E5          785      SCHRODER H C/AU
E6            5      SCHRODER H CH/AU
E7            1      SCHRODER H CORRECTED TO SCHODER H/AU
E8          410      SCHRODER H D/AU
E9            1      SCHRODER H D A A/AU
E10           1      SCHRODER H DAA/AU
E11         111      SCHRODER H E/AU
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=> s e3
L13        2098 "SCHRODER H"/AU

=> e zelder o/au
E1            2      ZELDER JOY B/AU
E2            1      ZELDER MARTIN/AU
E3          213 --> ZELDER O/AU
E4           83      ZELDER OSKAR/AU
E5            1      ZELDER S/AU
E6            1      ZELDER SUSANNE/AU
E7            1      ZELDER T R/AU
E8            2      ZELDERLOO L/AU
E9            1      ZELDERS F/AU
E10           1      ZELDERS H G/AU
E11           2      ZELDERS I T/AU
E12           2      ZELDERS N/AU

=> s e3-e4
L14         294 ("ZELDER O"/AU OR "ZELDER OSKAR"/AU)
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=> e haberhauer g/au
E1            2     HABERHAUER D/AU
E2            1     HABERHAUER F/AU
E3          249 --> HABERHAUER G/AU
E4           24     HABERHAUER GEBHARD/AU
E5           31     HABERHAUER GEORG/AU
E6            1     HABERHAUER GEORG F/AU
E7           22     HABERHAUER GREGOR/AU
E8            3     HABERHAUER GUENTHER/AU
E9            2     HABERHAUER GUNTHER/AU
E10           1     HABERHAUER HELMUT/AU
E11           5     HABERHAUER HELMUTH/AU
E12           1     HABERHAUER OSWALD/AU

=> s e3-e7
L15         327 ("HABERHAUER G"/AU OR "HABERHAUER GEBHARD"/AU OR "HABERHAUER
                GEORG"/AU OR "HABERHAUER GEORG F"/AU OR "HABERHAUER GREGOR"/AU)

=> d his

     (FILE 'HOME' ENTERED AT 10:28:20 ON 03 NOV 2004)

     FILE 'STNGUIDE' ENTERED AT 10:28:36 ON 03 NOV 2004

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 10:29:09 ON 03 NOV 2004
L1          3991 S SUGAR (A) PHOSPHOTRANSFERASE?
L2             0 S CORYNEBACTEROIM (A) GLUTAMICUM
L3          7436 S CORYNEBACTERIUM (A) GLUTAMICUM
L4            23 S L1 AND L3
L5            14 DUP REM L4 (9 DUPLICATES REMOVED)
L6         53493 S CORYNEBACTERIUM
L7            29 S L1 AND L6
L8       6771179 S CLON? OR EXPRESS? OR RECOMBINANT
L9            14 S L7 AND L8
L10            8 DUP REM L9 (6 DUPLICATES REMOVED)
                 E POMPEJUS M/AU
L11           85 S E3-E4
                 E KROGER K/AU
                 E KROGER B/AU
L12          132 S E3-E8
                 E SCHRODER H/AU
L13         2098 S E3
                 E ZELDER O/AU
L14          294 S E3-E4
                 E HABERHAUER G/AU
L15          327 S E3-E7

=> s l11 or l12 or l13 or l14 or l15
L16        2832 L11 OR L12 OR L13 OR L14 OR L15

=> s l1 and l16
L17           4 L1 AND L16

=> dup rem l17
PROCESSING COMPLETED FOR L17
L18           3 DUP REM L17 (1 DUPLICATE REMOVED)

=> d 1-3 ibib ab

L18  ANSWER 1 OF 3  EMBASE  COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
     on STN
ACCESSION NUMBER:   2004033592  EMBASE
TITLE:              Comparative Metabolic Flux Analysis of Lysine-Producing
```

Corynebacterium glutamicum Cultured on Glucose or Fructose.

AUTHOR: Kiefer P.; Heinzle E.; **Zelder O.**; Wittmann C.
CORPORATE SOURCE: C. Wittmann, Biochemical Engineering, Saarland University, Im Stadtwald, 66041 Saarbrucken, Germany. c.wittmann@mx.uni-saarland.de

SOURCE: Applied and Environmental Microbiology, (2004) 70/1 (229-239).
Refs: 22
ISSN: 0099-2240 CODEN: AEMIDF
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB A comprehensive approach to (13)C tracer studies, labeling measurements by gas chromatography-mass spectrometry, metabolite balancing, and isotopomer modeling, was applied for comparative metabolic network analysis of lysine-producing Corynebacterium glutamicum on glucose or fructose. Significantly reduced yields of lysine and biomass and enhanced formation of dihydroxyacetone, glycerol, and lactate in comparison to those for glucose resulted on fructose. Metabolic flux analysis revealed drastic differences in intracellular flux depending on the carbon source applied. On fructose, flux through the pentose phosphate pathway (PPP) was only 14.4% of the total substrate uptake flux and therefore markedly decreased compared to that for glucose (62.0%). This result is due mainly to (i) the predominance of phosphoenolpyruvate-dependent phosphotransferase systems for fructose uptake (PTS(Fructose)) (92.3%), resulting in a major entry of fructose via fructose 1,6-bisphosphate, and (ii) the inactivity of fructose 1,6-bisphosphatase (0.0%). The uptake of fructose during flux via PTS (Mannose) was only 7.7%. In glucose-grown cells, the flux through pyruvate dehydrogenase (70.9%) was much less than that in fructose-grown cells (95.2%). Accordingly, flux through the tricarboxylic acid cycle was decreased on glucose. Normalized to that for glucose uptake, the supply of NADPH during flux was only 112.4% on fructose compared to 176.9% on glucose, which might explain the substantially lower lysine yield of C. glutamicum on fructose. Balancing NADPH levels even revealed an apparent deficiency of NADPH on fructose, which is probably overcome by in vivo activity of malic enzyme. Based on these results, potential targets could be identified for optimization of lysine production by C. glutamicum on fructose, involving (i) modification of flux through the two PTS for fructose uptake, (ii) amplification of fructose 1,6-bisphosphatase to increase flux through the PPP, and (iii) knockout of a not-yet-annotated gene encoding dihydroxyacetone phosphatase or kinase activity to suppress overflow metabolism. Statistical evaluation revealed high precision of the estimates of flux, so the observed differences for metabolic flux are clearly substrate specific.

L18 ANSWER 2 OF 3 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:377040 HCAPLUS
DOCUMENT NUMBER: 138:380496
TITLE: Genes coding for components of the phosphoenolpyruvate-**sugar**-**phosphotransferase** system and their use in engineering of microbial metabolism
INVENTOR(S): **Zelder, Oskar**; **Pompejus, Markus**; Schroeder, Hartwig; Kroeger, Burkhard; Klopprogge, Corinna; **Haberhauer, Gregor**
PATENT ASSIGNEE(S): BASF Aktiengesellschaft, Germany
SOURCE: PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003040357	A2	20030515	WO 2002-EP12140	20021031
WO 2003040357	A3	20031224		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

DE 10154276	A1	20030515	DE 2001-10154276	20011105
EP 1444334	A2	20040811	EP 2002-783045	20021031

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK

PRIORITY APPLN. INFO.:	DE 2001-10154276	A	20011105
	WO 2002-EP12140	W	20021031

AB The invention relates to novel nucleic acid mols., the use thereof in the construction of bio-engineered improved microorganisms and to methods for the production of fine chems., especially amino acids with the aid of said bio-engineered improved microorganisms. Genes for components of the phosphoenolpyruvate-**sugar-phosphotransferase** system od Corynebacterium glutamicum are identified. The enzymes and genes may be useful in manipulating sugar uptake and metabolism in microorganisms to alter their energy metabolism and fermentation properties (no data.).

L18 ANSWER 3 OF 3 BIOTECHDS COPYRIGHT 2004 THE THOMSON CORP. on STN
DUPLICATE 1

ACCESSION NUMBER: 2001-04894 BIOTECHDS

TITLE: Corynebacterium glutamicum nucleic acids encoding phosphoenolpyruvate:**sugar phosphotransferase** system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation; selectable marker

AUTHOR: **Pompejus M**; Kroeger B; Schroeder H; **Zelder O**; **Haberhauer G**

PATENT ASSIGNEE: BASF

LOCATION: Ludwigshafen, Germany.

PATENT INFO: WO 2001002583 11 Jan 2001

APPLICATION INFO: WO 2000-DE973 27 Jun 2000

PRIORITY INFO: DE 1999-1042097 3 Sep 1999; US 1999-142691 1 Jul 1999

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2001-080989 [09]

AB Isolated Corynebacterium glutamicum ATCC 13032 nucleic acids encoding phosphoenolpyruvate:**sugar-phosphotransferase** system (PTS) proteins or their fragments are claimed. A PTS nucleic acid (N1) does not consist of any of the F-designated genes defined and is selected from one of 17 disclosed nucleic acid sequences (S1) and their fragments nucleic acid which encode a protein selected from one of the 17 protein sequences (S2) disclosed; nucleic acid encoding a naturally occurring allelic variant of a protein selected from (S2). Also claimed are methods for producing the proteins; C. glutamicum PTS protein and its fragments; diagnosis of Corynebacterium diphtheriae infection; fusion proteins; antisense PTS nucleic acid; a method for screening molecules which modulate the activity of a PTS protein; and a transformed host cell. (144pp)

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     (FILE 'HOME' ENTERED AT 10:28:20 ON 03 NOV 2004)

     FILE 'STNGUIDE' ENTERED AT 10:28:36 ON 03 NOV 2004

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 10:29:09 ON 03 NOV 2004
L1          3991 S SUGAR (A) PHOSPHOTRANSFERASE?
L2             0 S CORYNEBACTEROIM (A) GLUTAMICUM
L3          7436 S CORYNEBACTERIUM (A) GLUTAMICUM
L4            23 S L1 AND L3
L5            14 DUP REM L4 (9 DUPLICATES REMOVED)
L6         53493 S CORYNEBACTERIUM
L7            29 S L1 AND L6
L8       6771179 S CLON? OR EXPRESS? OR RECOMBINANT
L9            14 S L7 AND L8
L10            8 DUP REM L9 (6 DUPLICATES REMOVED)
                 E POMPEJUS M/AU
L11           85 S E3-E4
                 E KROGER K/AU
                 E KROGER B/AU
L12          132 S E3-E8
                 E SCHRODER H/AU
L13         2098 S E3
                 E ZELDER O/AU
L14          294 S E3-E4
                 E HABERHAUER G/AU
L15          327 S E3-E7
L16         2832 S L11 OR L12 OR L13 OR L14 OR L15
L17            4 S L1 AND L16
L18            3 DUP REM L17 (1 DUPLICATE REMOVED)
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	Issue Date	Pages	Document ID	Title
1	20021226	158	US 20020197605 A1	Novel Polynucleotides

	Issue Date	Pages	Document ID	Title
1	20030123	40	US 20030017495 A1	Enterococcus faecalis polynucleotides and polypeptides
2	20021024	26	US 20020155521 A1	APPLICATION OF GLUCOSE TRANSPORT MUTANTS FOR PRODUCTION OF AROMATIC PATHWAY COMPOUNDS
3	20020314	64	US 20020032323 A1	STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES
4	20040817	23	US 6777176 B1	Target system
5	20030624	243	US 6583275 B1	Nucleic acid sequences and expression system relating to Enterococcus faecium for diagnostics and therapeutics
6	20011113	11	US 6316232 B1	Microbial preparation of substances from aromatic metabolism/I

	L #	Hits	Search Text
1	L1	129	sugar adj phosphotransferase$2
2	L2	9866	corynebacterium
3	L3	1	l1 same l2
4	L4	673073	clon$3 or express$3 or recombinant
5	L5	6	l1 same l4
6	L6	7096	POMPEJUS KROGER sCHRODER ZELDERZEL DERHABERHAUER
7	L7	0	l1 and l6

	Issue Date	Pages	Document ID	Title
1	20040304	98	US 20040043953 A1	Genes of corynebacterium
2	20031204	78	US 20030224415 A1	Selection free growth of host cells containing multiple integrating vectors
3	20030918	62	US 20030176652 A1	Human and mouse beta-defensins, antimicrobial peptides
4	20030515	109	US 20030092882 A1	Host cells containing multiple integrating vectors
5	20030313	214	US 20030049804 A1	Corynebacterium glutamicum genes encoding metabolic pathway proteins
6	20040224	258	US 6696561 B1	Corynebacterium glutamicum genes encoding proteins involved in membrane synthesis and membrane transport
7	20000808	38	US 6100453 A	Transgenic pomaceous fruit with fire blight resistance
8	19981020	39	US 5824861 A	Transgenic pomaceous fruit with fire blight resistance